

FIGURE 1

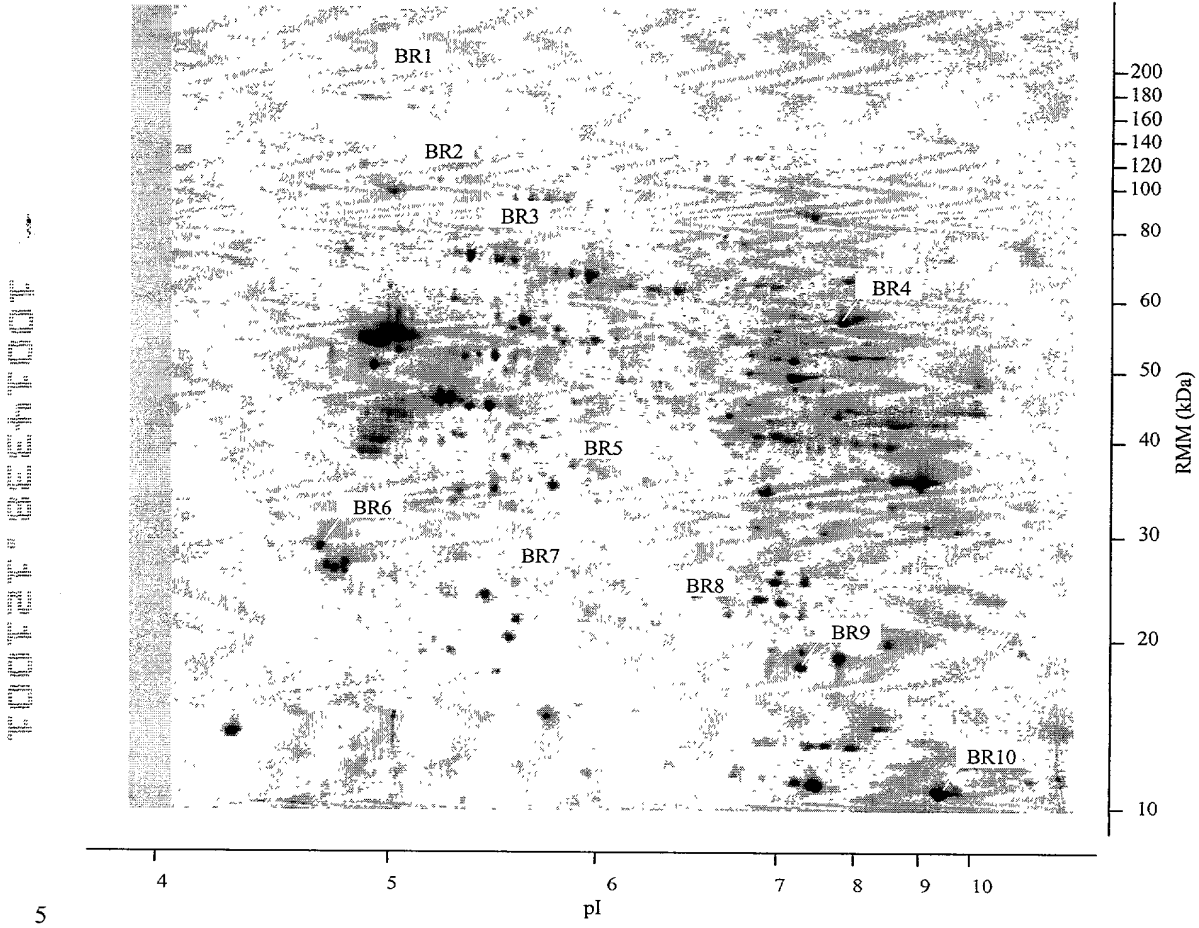


FIGURE 2.

Figure 2a

1 gtccgggacc atgtctggag aactaccacc aaacattaac atcaaggaac
5 51 ctcgatggga tcaaagcact ttcattggac gagccaatca tttcttcact
101 gtaactgacc ccaggaacat tctgttaacc aacgaacaac tcgagagtgc
151 gagaaaaata gtacatgatt acaggcaagg aattgttcct cctggtctta
201 cagaaaatga attgtggaga gcaaagtaca tctatgattc agcttttcat
251 cctgacactg gtgagaagat gattttgata ggaagaatgt cagcccaggt
10 301 tcccatgaac atgaccatca caggttgtat gatgacgttt tacaggacta
351 cgccggctgt gctgttctgg cagtggatta accagtcctt caatgccgtc
401 gtcaattaca ccaacagaag tggagacgca cccctcactg tcaatgagtt
451 gggaacagct tacgtttctg caacaactgg tgccgtagca acagctctag
501 gactcaatgc attgaccaag catgtctcac cactgatagg acgttttggt
45 551 ccctttgctg ccgtagctgc tgctaattgc attaatattc cattaatgag
601 gcaaaggga ctcaaagttg gcattcccgt cacggatgag aatgggaacc
651 gcttggggga gtcggcgaac gctgcgaaac aagccatcac gcaagttgtc
701 gtgtccagga ttctcatggc agcccctggc atggccatcc ctccattcat
751 tatgaacact ttggaaaaga aagccttttt gaagagggtc ccatggatga
20 801 gtgcacccat tcaagttggg ttagttggct tctgtttggt gtttgctaca
851 cccctgtgtt gtgccctgtt tcctcagaaa agttccatgt ctgtgacaag
901 cttggaggcc gagttgcaag ctaagatcca agagagccat cctgaattgc
951 gacgcgtgta cttcaataag ggattgtaaa gcaggaggga aacctctgca
1001 gctcattctg ccactgcaaa gctgggtgtag ccatgctggt gagaaaaatc
25 1051 ctgttcaacc tgggttctcc cagttacgga aagggcgaat tcgcgccgcg
1101 taattcgatt cgccctatag nagtngtaac antc

Figure 2b

1 MSGELPPNIN IKEPRWDQST FIGRANHFFT VTDPRNILLT NEQLESARKI
51 VHDYRQGIVP PGLTENELWR AKYIYDSAHH PDTGEKMILI GRMSAQVPMN
5 101 MTITGCMMPF YRTTPAVLFW QWINQSFNAV VNYTNRSGDA PLTVNELGTA
151 YVSATTGAVA TALGLNALTK HVSPLIGRFV PFAAVAAANC INIPLMRQRE
201 LKVGIPVTDE NGNRLGESAN AAKQAITQVV VSRILMAAPG MAIPPFIMNT
251 LEKKAFLKRF PWMSAPIQVG LVGECLVFAT PLCCALFPQK SSMSVTSLEA
301 ELQAKIQESH PELRRVYFNK GL*

- 10 The tryptic peptides identified by mass spectrometry are underlined, motifs conserved in mouse sideroflexin 1 are boxed and sequences shaded in grey represent predicted transmembrane domains (Fleming *supra*)

FIGURE 3.

Figure 3a

1 gtccgggacc atgtctggag aactaccacc aaacattaac atcaaggaac
5 51 ctcgatggga tcaaagcact ttcattggac gagccaatca tttcttcact
101 gtaactgacc ccaggaacat tctgttaacc aacgaacaac tcgagagtgc
151 gagaaaaata gtacatgatt acaggcaagg aattgttcct cctgggtctta
201 cagaaaatga attgtggaga gcaaagtaca tctatgattc agcttttcat
251 cctgacactg gtgagaagat gattttgata ggaagaatgt cagcccaggt
301 tcccatgaac atgaccatca caggttgtat gatgacgttt tacaggacta
351 cgccggctgt gctgttctgg cagtggatta accagtcctt caatgccgtc
401 gtcaattaca ccaacagaag tggagacgca cccctcactg tcaatgagtt
451 gggaacagct tacgtttctg taacaactgg tgccgtagca acagctctag
501 gactcaatgc attgaccaag catgtctcac cactgatagg acgttttggt
551 ccctttgctg ccgtagctgc tgctaattgc attaatatc cattaatgag
601 gcaaagccat ccctccattc attatgaaca ctttggaaaa gaaagccttt
651 ttgaagaggt tcccatggat gagtgcaccc attcaagttg ggtagttgg
701 cttctgtttg gtgtttgcta caccctgtg ttgtgcctg tttcctcaga
751 aaagttccat gtctgtgaca agcttggagg ccgagttgca agctaagatc
801 caagagagcc atcctgaatt gcgacgctg tacttcaata agggattgta
851 aagcagggag gaaacctctg cagctcattc tgccactgca aagctggtgt
901 agccatgctg gtgagaaaaa tcctgttcaa cctgggttct cccagttang
951 gaaagggcga attcgcggcc gctgattcna ttac

Figure 3b

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5  1  MSGELPPNIN IKEPRWDQST FIGRANHFFT VTDPRNILLT NEQLESARKI
51  VHDYRQGIVP PGLTENELWR AKYIYDSAHH PDTGEKMILI GRMSAQVPMN
101 MPITGCMMPF YRTTPAVIEW OWINOSFNAV VNYTNRSGDA PLTVNELGTA
151 YVSVTTGAVA TALGLNALTK HVSPLIGRFV PFAAVAAANC INIPLMRQSH
201 PSIHYEHFGK ESLFEEVPMD ECTHSSWVSW LLFGVCYTPV LCPVSSEKFH
10 251 VCDKLGRVA S*

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The tryptic peptides identified by mass spectrometry are underlined, motifs conserved in mouse sideroflexin 1 are boxed and amino acids unique to this clone are shown in bold (all other amino acids are identical to the full length clone), sequences shaded in grey represent the predicted transmembrane domains.